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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/080,233

DATE: 03/13/2002

TIME: 15:11:42

Input Set : A:\GC567-SEQLIST.txt

Output Set: N:\CRF3\03132002\J080233.raw

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4 <110> APPLICANT: Wang, Huaming
6 <120> TITLE OF INVENTION: Novel Phenol Oxidizing Enzymes
9 <130> FILE REFERENCE: GC567
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/080,233
C--> 12 <141> CURRENT FILING DATE: 2002-02-19
14 <160> NUMBER OF SEQ ID NOS: 5
16 <170> SOFTWARE: FastSEQ for Windows Version 4.0
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 1791
20 <212> TYPE: DNA
21 <213> ORGANISM: Stachybotrys sp.
23 <400> SEQUENCE: 1
24 gtcaatatgc tgttcaagtc atggcaactg gcagcagcct ccgggctcct gtctggagtc      60
25 ctccggcatcc cgatggacac cggcagccac cccattgagg ctgttgatcc cgaagtgaag      120
26 actgaggctct tcgctgactc cctccttgcg gcagcaggcg atgacgactg ggagtcacct      180
27 ccatacaact tgctttacag gaatgccctg ccaattccac ctgtcaagca gcccaagatg      240
28 atcattacca accctgtcac cggcaaggac atttggtact atgagatcga gatcaagcca      300
29 tttcagcaaa ggatttacct cacttgcgc cctgccactc tcgtcggcta cgatggcatg      360
30 agccctgggtc ctactttcaa tgttcccaga ggaacagaga ctgtagttag gttcatcaac      420
31 aatgccaccg tggagaactc ggtccatctg cacggctccc catcgctgc ccctttcgat      480
32 ggttgggctg aagatgtgac ctccctggc gagtacaagg attactactt tcccaactac      540
33 caatccgccc gccttctgtg gtaccatgac cacgctttca tgaagactgc tgagaatgcc      600
34 tactttggtc aggtggcgc ctacattatc aacgacgagg ctgaggatgc tctcgggtctt      660
35 cctagtggct atggcgagtt cgatatccct ctgatcctga cggccaagta ctataacgcc      720
36 gatggtaccc tgcgttcgac cgaggggtgag gaccaggacc tgtggggaga tgtcatccat      780
37 gtcaacggac agccatggcc ttcccttaac gtccagcccc gcaagtaccg ttcccgattc      840
38 ctcaacgctg ccgtgtctcg tgccttggctc ctctacctcg tcaggaccag ctctcccaac      900
39 gtcagaattc ctttccaagt cattgcctct gatgctggtc tccttcaagc ccccgttcag      960
40 acctctaacc tctaccttgc tgttgccgag gtttacgaga tcattattga cttcaccaac     1020
41 tttgctggcc agactcttga cctgcgcaac gttgctgaga ccaacgatgt cggcgacgag     1080
42 gatgagtacg ctgcactctc cgaggtgatg cgcttcgtcg tcagctctgg cactgttgag     1140
43 gacaacagcc aggtcccttc cactctccgt gacgttccct tccctcctca caaggaaggc     1200
44 cccgccgaca agcaattcaa gtttgaacgc agcaacggac actacctgat caacgatgtt     1260
45 ggctttgccg atgtcaatga gcgtgtcctg gccaaagccc agctcggcac cgttgaggtc     1320
46 tgggagctcg agaactctc tggaggctgg agccacccc tccacattca ccttggtgac     1380
47 ttcaagatcc tcaagcgaac tgggtgctgt ggccaggtea tgccctacga gtctgctggt     1440
48 cttaaggatg tcgtctggtt gggcaggggt gagaccctga ccatcgaggc ccactaccaa     1500
49 ccctggactg gagcttacat gtggcactgt cacaacctca ttcacgagga taacgacatg     1560
50 atggctgtat tcaacgtcac cgccatggag gagaagggat atcttcagga ggacttcgag     1620
51 gaccccatga accccaagtg gcgcgcggtt ccttacaacc gcaacgactt ccattgctgc     1680
52 gctggaaact tctccgccga gtccatcact gcccgagtgc aggagctggc cgagcaggag     1740
53 ccgtacaacc gcctcgatga gatcctggag gatcttggaa tcgaggagta a              1791
55 <210> SEQ ID NO: 2

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56 <211> LENGTH: 594
57 <212> TYPE: PRT
58 <213> ORGANISM: Stachybotrys sp.
60 <400> SEQUENCE: 2
61 Met Leu Phe Lys Ser Trp Gln Leu Ala Ala Ala Ser Gly Leu Leu Ser
62 1 5 10 15
63 Gly Val Leu Gly Ile Pro Met Asp Thr Gly Ser His Pro Ile Glu Ala
64 20 25 30
65 Val Asp Pro Glu Val Lys Thr Glu Val Phe Ala Asp Ser Leu Leu Ala
66 35 40 45
67 Ala Ala Gly Asp Asp Asp Trp Glu Ser Pro Pro Tyr Asn Leu Leu Tyr
68 50 55 60
69 Arg Asn Ala Leu Pro Ile Pro Pro Val Lys Gln Pro Lys Met Ile Ile
70 65 70 75 80
71 Thr Asn Pro Val Thr Gly Lys Asp Ile Trp Tyr Tyr Glu Ile Glu Ile
72 85 90 95
73 Lys Pro Phe Gln Gln Arg Ile Tyr Pro Thr Leu Arg Pro Ala Thr Leu
74 100 105 110
75 Val Gly Tyr Asp Gly Met Ser Pro Gly Pro Thr Phe Asn Val Pro Arg
76 115 120 125
77 Gly Thr Glu Thr Val Val Arg Phe Ile Asn Asn Ala Thr Val Glu Asn
78 130 135 140
79 Ser Val His Leu His Gly Ser Pro Ser Arg Ala Pro Phe Asp Gly Trp
80 145 150 155 160
81 Ala Glu Asp Val Thr Phe Pro Gly Glu Tyr Lys Asp Tyr Tyr Phe Pro
82 165 170 175
83 Asn Tyr Gln Ser Ala Arg Leu Leu Trp Tyr His Asp His Ala Phe Met
84 180 185 190
85 Lys Thr Ala Glu Asn Ala Tyr Phe Gly Gln Ala Gly Ala Tyr Ile Ile
86 195 200 205
87 Asn Asp Glu Ala Glu Asp Ala Leu Gly Leu Pro Ser Gly Tyr Gly Glu
88 210 215 220
89 Phe Asp Ile Pro Leu Ile Leu Thr Ala Lys Tyr Tyr Asn Ala Asp Gly
90 225 230 235 240
91 Thr Leu Arg Ser Thr Glu Gly Glu Asp Gln Asp Leu Trp Gly Asp Val
92 245 250 255
93 Ile His Val Asn Gly Gln Pro Trp Pro Phe Leu Asn Val Gln Pro Arg
94 260 265 270
95 Lys Tyr Arg Phe Arg Phe Leu Asn Ala Ala Val Ser Arg Ala Trp Leu
96 275 280 285
97 Leu Tyr Leu Val Arg Thr Ser Ser Pro Asn Val Arg Ile Pro Phe Gln
98 290 295 300
99 Val Ile Ala Ser Asp Ala Gly Leu Leu Gln Ala Pro Val Gln Thr Ser
100 305 310 315 320
101 Asn Leu Tyr Leu Ala Val Ala Glu Arg Tyr Glu Ile Ile Ile Asp Phe
102 325 330 335
103 Thr Asn Phe Ala Gly Gln Thr Leu Asp Leu Arg Asn Val Ala Glu Thr
104 340 345 350
105 Asn Asp Val Gly Asp Glu Asp Glu Tyr Ala Arg Thr Leu Glu Val Met

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106          355          360          365
107 Arg Phe Val Val Ser Ser Gly Thr Val Glu Asp Asn Ser Gln Val Pro
108          370          375          380
109 Ser Thr Leu Arg Asp Val Pro Phe Pro Pro His Lys Glu Gly Pro Ala
110 385          390          395          400
111 Asp Lys His Phe Lys Phe Glu Arg Ser Asn Gly His Tyr Leu Ile Asn
112          405          410          415
113 Asp Val Gly Phe Ala Asp Val Asn Glu Arg Val Leu Ala Lys Pro Glu
114          420          425          430
115 Leu Gly Thr Val Glu Val Trp Glu Leu Glu Asn Ser Ser Gly Gly Trp
116          435          440          445
117 Ser His Pro Val His Ile His Leu Val Asp Phe Lys Ile Leu Lys Arg
118          450          455          460
119 Thr Gly Gly Arg Gly Gln Val Met Pro Tyr Glu Ser Ala Gly Leu Lys
120 465          470          475          480
121 Asp Val Val Trp Leu Gly Arg Gly Glu Thr Leu Thr Ile Glu Ala His
122          485          490          495
123 Tyr Gln Pro Trp Thr Gly Ala Tyr Met Trp His Cys His Asn Leu Ile
124          500          505          510
125 His Glu Asp Asn Asp Met Met Ala Val Phe Asn Val Thr Ala Met Glu
126          515          520          525
127 Glu Lys Gly Tyr Leu Gln Glu Asp Phe Glu Asp Pro Met Asn Pro Lys
128          530          535          540
129 Trp Arg Ala Val Pro Tyr Asn Arg Asn Asp Phe His Ala Arg Ala Gly
130 545          550          555          560
131 Asn Phe Ser Ala Glu Ser Ile Thr Ala Arg Val Gln Glu Leu Ala Glu
132          565          570          575
133 Gln Glu Pro Tyr Asn Arg Leu Asp Glu Ile Leu Glu Asp Leu Gly Ile
134          580          585          590
135 Glu Glu
138 <210> SEQ ID NO: 3
139 <211> LENGTH: 3677
140 <212> TYPE: DNA
141 <213> ORGANISM: Stachybotrys chartarum
143 <400> SEQUENCE: 3
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145 agtcaatata ttggtcactg ctaatagttc cttgctacgc gcaaaaagct ccttgccgaa      120
146 ggggcacaga ctatcaagtg agacatatag gatgcatgtc tttcatagcc acagttaggg      180
147 tgggtgacct ctcgaagagg ccccgacttg catgcatacg acatgtcgct tccatgcaac      240
148 atgtatgcgc acatcggcga tcaggcaccc tctgcatgca gaatagaacc cccctggttt      300
149 ccttttgttt cttttccttt ctcaacgacg cgtgagcgtg gttaacttga gcaaggccga      360
150 gtggtctgtt cactgaggtt ccatcgaact ctcttctttt ccaatcatga cctgcccccc      420
151 gagtttagcc cccatcacgg ctgtgaaatc cacttcgata atcctagcct agtgctactc      480
152 ttcaatagtt gctcctgatg gggcactttg gtcacattgc cttggttyct cctacctcgt      540
153 tctcttcgcg atcaagcctc tatgcccgcg gacaacacct cattggcccg gaccactttg      600
154 agcgcgcacg caccttcgcg ccgaaggagt tgataacacc cttcaccctt gcccaatgat      660
155 ggagtttttg tctatttgtc atgatcacct cacattcact agatcacgga tcctggaaga      720
156 ggggtgtggaa gccagaccag cttgtccctg ttcttgacga ctcaggtcag ctcctagcgg      780
157 ctatcacagc tcaggattat caagtcccggt aaagtccaga cccttttcat tgtatgatgc      840

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158 tgcctaattt gcgctatctc tatgcgctag cagcgcgtctt ggctacaact ggctgccatg      900
159 gctgaagcat cgtgagatct ataaaggtct ccgaatcctc ggtgaagtca gaatcgtctc      960
160 tccacaccag tcaacaacaa gcttctttct cttacagctt agcctgagca cattcacaga    1020
161 actcttccct tcttttcgtc aatatgctgt tcaagtcatt gcaactggca gcagcctccg    1080
162 ggctcctgtc tggagtcctc ggcatcccga tggacaccgg cagccacccc attgaggctg    1140
163 ttgatcccga agtgaagact gaggtcttcg ctgactccct ccttgctgca gcaggcgatg    1200
164 acgactggga gtcacctcca tacaacttgc ttacagggtg agacacctgt cccacctgtt    1260
165 ttccctcgat aactaactct tataggaatg cctggccaat tccacctgtc aagcagccca    1320
166 agatgtatgt ctttgatttt ctacgaagca actcggcccc gactaatgta ttctaggatc    1380
167 attaccaacc ctgtcaccgg caaggacatt tggtagctat agatcgagat caagccattt    1440
168 cagcaaaggg tgagtttgct cagaaacctt gtggttaatta atcattgtta ctgacccttt    1500
169 cagattttacc ccaccttgcg ccttgccact ctogtcgggt acgatggcat gagccctggt    1560
170 cctactttca atgttcccag aggaacagag actgtagtta ggttcatcaa caatgccacc    1620
171 gtggagaact cgggtccatct gcacggtctc ccctcggctg ccccttttga tggttgggct    1680
172 gaagatgtga ccttccctgg cgagtacaag gattactact ttcccaacta ccaatccgcc    1740
173 cgccttctgt ggtaccatga ccacgcttct atgaaggtat gctacgagcc ttatcttttc    1800
174 ttggtacct ttggttaacc aacttccctt cgtagactgc tgagaatgcc tactttggtc    1860
175 aggtggcgcg ctacattatc aacgacgagg ctgaggatgc tctcggctct ctagtggtct    1920
176 atggcgagtt cgatatccct ctgatccctga cggcccaagta ctataacgcc gatggtaacc    1980
177 tgcgttcgac caggggtgag gaccaggacc tgtggggaga tgtcatccat gtcaacggac    2040
178 agccatggcc ttctcttaac gtccagcccc gcaagtagcg ttctcgatct ctcaacgctg    2100
179 cgtgtctctg tgcttggtct ctctacctcg tcaggaccag ctctcccaac gtcagaattc    2160
180 ctttccaagt cattgcctct gatgtgggtc tcttcaagc ccccgttcag acctctaacc    2220
181 tctaccttgc tgttgccgag cgttacgaga tcattattgg tatgccctcc cctctcagca    2280
182 atgagtcaag aactctaaga ctaacacttg tagacttcac caactttgct ggccagactc    2340
183 ttgacctgcg caacggttct gagaccaacg atgtcggcga cgaggatgag tacgtctgca    2400
184 ctctcgaggt gatgcgcttc gtctcagct ctggcactgt tgaggacaac agccaggctc    2460
185 cctccactct cgtgacgtt cctttccctc ctcaacagga aggccccgcc gacaagcact    2520
186 tcaagtttga acgcagcaac ggacactacc tgatcaacga tgttggtctt gccgatgtca    2580
187 atgagcgtgt cctggccaag ccagagctcg gcaccgttga ggtctgggag ctcgagaact    2640
188 cctctggagg ctggagccac ccggtccaca ttacacttgt tgacttcaag atcctcaagc    2700
189 gaactgggtg tcgtggccag gtcattgcct acgagtctgc tgggtcttaag gatgtcgtct    2760
190 ggttgggcag ggtgagacc ctgacctcag aggcccaact ccaacctgga actggagctt    2820
191 acatgtggca ctgtcacaac ctcatcagc aggataacga catgatggct gtattcaacg    2880
192 tcaccgccat ggaggagaag ggatatcttc aggaggactt cgaggacccc atgaacccca    2940
193 agtggcgcgc cgttccctac aaccgcaacg acttccatgc tcgcgctgga aacttctccg    3000
194 ccgagtcctc cactgcccga gtgcaggagc tggccgagca ggagccgtac aaccgctcg    3060
195 atgagatcct ggaggatctt ggaatcgagg agtaaaccoc gagccacaag ctctacaatc    3120
196 gttttgagtc ttaagacgag gctcttggtg cgtattcttt tcttccctac ggggaactcc    3180
197 gctgtccact gcgatgtgaa ggaccatcac aaagcaacgt atatatggga ctaccactg    3240
198 tcattaccgc ccacttgtac ctattcgatt cttgttcaaa cttttctagt gcgagagtgt    3300
199 ccatagtcaa gaaacgcccc tagggctatc gtctaaactg aactatttggt tggctctgta    3360
200 cgtggagtag atgtcaattg tgatgagaca cagtaaatac ggtatatctt ttctaggac    3420
201 tacaggatca gtttctcatg agattacatc cgtctaatgt ttgtccatga gagtctagct    3480
202 aaggttgaga atgcacaga cggaatcatt tgatgctctc agctcgtatt accgatgtaa    3540
203 gacaagttag gtaagttgct tggtatccga aaatgactca ggctccctca ttaggttgca    3600
204 tgtgaaaacc ttacagcaact catgggtgtt gggaccaaact catccatacc tgattttgat    3660
205 aactgacctg ggtcaat                                     3677
207 <210> SEQ ID NO: 4

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Input Set : A:\GC567-SEQLIST.txt

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208 &lt;211&gt; LENGTH: 568

209 &lt;212&gt; TYPE: PRT

210 &lt;213&gt; ORGANISM: Bilirubin oxidase

212 &lt;400&gt; SEQUENCE: 4

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213 Met Phe Lys His Thr Leu Gly Ala Ala Ala Leu Ser Leu Leu Phe Asn
214   1           5           10           15
215 Ser Asn Ala Val Gln Ala Ser Pro Val Pro Glu Thr Ser Pro Ala Thr
216           20           25           30
217 Gly His Leu Phe Lys Arg Val Ala Gln Ile Ser Pro Gln Tyr Pro Met
218           35           40           45
219 Phe Thr Val Pro Leu Pro Ile Pro Pro Val Lys Gln Pro Arg Leu Thr
220           50           55           60
221 Val Thr Asn Pro Val Asn Gly Gln Glu Ile Trp Tyr Tyr Glu Val Glu
222 65           70           75           80
223 Ile Lys Pro Phe Thr His Gln Val Tyr Pro Asp Leu Gly Ser Ala Asp
224           85           90           95
225 Leu Val Gly Tyr Asp Gly Met Ser Pro Gly Pro Thr Phe Gln Val Pro
226           100          105          110
227 Arg Gly Val Glu Thr Val Val Arg Phe Ile Asn Asn Ala Glu Ala Pro
228           115          120          125
229 Asn Ser Val His Leu His Gly Ser Phe Ser Arg Ala Ala Phe Asp Gly
230           130          135          140
231 Trp Ala Glu Asp Ile Thr Glu Pro Gly Ser Phe Lys Asp Tyr Tyr Tyr
232 145          150          155          160
233 Pro Asn Arg Gln Ser Ala Arg Thr Leu Trp Tyr His Asp His Ala Met
234           165          170          175
235 His Ile Thr Ala Glu Asn Ala Tyr Arg Gly Gln Ala Gly Leu Tyr Met
236           180          185          190
237 Leu Thr Asp Pro Ala Glu Asp Ala Leu Asn Leu Pro Ser Gly Tyr Gly
238           195          200          205
239 Glu Phe Asp Ile Pro Met Ile Leu Thr Ser Lys Gln Tyr Thr Ala Asn
240           210          215          220
241 Gly Asn Leu Val Thr Thr Asn Gly Glu Leu Asn Ser Phe Trp Gly Asp
242 225          230          235          240
243 Val Ile His Val Asn Gly Gln Pro Trp Pro Phe Lys Asn Val Glu Pro
244           245          250          255
245 Arg Lys Tyr Arg Phe Arg Phe Leu Asp Ala Ala Val Ser Arg Ser Phe
246           260          265          270
247 Gly Leu Tyr Phe Ala Asp Thr Asp Ala Ile Asp Thr Arg Leu Pro Phe
248           275          280          285
249 Lys Val Ile Ala Ser Asp Ser Gly Leu Leu Glu His Pro Ala Asp Thr
250           290          295          300
251 Ser Leu Leu Tyr Ile Ser Met Ala Glu Arg Tyr Glu Val Val Phe Asp
252 305          310          315          320
253 Phe Ser Asp Tyr Ala Gly Lys Thr Ile Glu Leu Arg Asn Leu Gly Gly
254           325          330          335
255 Ser Ile Gly Gly Ile Gly Thr Asp Thr Asp Tyr Asp Asn Thr Asp Lys
256           340          345          350
257 Val Met Arg Phe Val Val Ala Asp Asp Thr Thr Gln Pro Asp Thr Ser

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**VERIFICATION SUMMARY**

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Input Set : A:\GC567-SEQLIST.txt

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L:11 M:270 C: Current Application Number differs, Replaced Current Application Number

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date